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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/932,367A

DATE: 02/13/2002

TIME: 18:44:29

Input Set : A:\053844-5003.txt

Output Set: N:\CRF3\02132002\I932367A.raw

ENTERED
see page 5

3 <110> APPLICANT: RHODES, Simon J.
4 BRIDWELL, Jeanne L.
5 MEIER, Bradley C.
6 PARKER, Gretchen E.
7 PRICE, Jeffrey R.
8 SHOWALTER, Aaron D.
9 SLOOP, Kyle W.
11 <120> TITLE OF INVENTION: GENERATION OF DIAGNOSTIC TOOLS TO ASSAY THE HUMAN
12 LHX3/P-LIM/LIM-3 FACTOR
14 <130> FILE REFERENCE: 053884-5003
16 <140> CURRENT APPLICATION NUMBER: 09/932,367A
17 <141> CURRENT FILING DATE: 2001-08-17
19 <150> PRIOR APPLICATION NUMBER: PCT/US00/04424
20 <151> PRIOR FILING DATE: 2000-02-22
22 <150> PRIOR APPLICATION NUMBER: US 60/121,110
23 <151> PRIOR FILING DATE: 1999-02-22
25 <160> NUMBER OF SEQ ID NOS: 113
27 <170> SOFTWARE: PatentIn Ver. 2.1
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 1605
31 <212> TYPE: DNA
32 <213> ORGANISM: Sus scrofa
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37 cctcaagtgc agtgactgcc acacgcgcgt ggccgagcgc tgcttcagcc gcggagagag 180
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41 ggacagcccg ctcgtgtgca aggcgcacta cgagaccgcc aagcagcgag aggcggaggc 420
42 cacggccaag cgcccgcgca cgaccatcac ggccaagcag ctggagacgc tgaagagcgc 480
43 ctacaacacg tcgcccagc ccgcgcgcca cgtgcgcgag cagctctcct ccgagaccgg 540
44 cctggacatg cgcgtcgtgc aggtgtggtt ccagaaccgc cgggccaagg aaaagcggct 600
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47 ggtctccttc acagacgagc catccatggc cgaaatgggc cctgccaacg gcctctacgg 780
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52 gccccaccc atgaggggtg tggcagggaa cggaccacgc tccgacctat ccacggggag 1080
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54 cgctcagttc tgactgaggc cccagctccg tggagcacca gacacgagca ctgcccctgg 1200

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57 ggactttctc ccggtctcga ggctccttct gggacaaggg gagccacctg gtggctgctc 1380
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59 gctgctcttt ctagaccgga gtggtcagcc cccgaagccg gggagggggg ctctccccag 1500
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65 <211> LENGTH: 383
66 <212> TYPE: PRT
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71 1 5 10 15
73 Ala Gly Cys Asp Gln His Ile Leu Asp Arg Phe Ile Leu Lys Ala Leu
74 20 25 30
76 Asp Arg His Trp His Ser Lys Cys Leu Lys Cys Ser Asp Cys His Thr
77 35 40 45
79 Pro Leu Ala Glu Arg Cys Phe Ser Arg Gly Glu Ser Leu Tyr Cys Lys
80 50 55 60
82 Asp Asp Phe Phe Lys Arg Phe Gly Thr Lys Cys Ala Ala Cys Gln Leu
83 65 70 75 80
85 Gly Ile Pro Pro Thr Gln Val Val Arg Arg Ala Gln Asp Phe Val Tyr
86 85 90 95
88 His Leu His Cys Phe Ala Cys Val Val Cys Lys Arg Gln Leu Ala Thr
89 100 105 110
91 Gly Asp Glu Phe Tyr Leu Met Glu Asp Ser Arg Leu Val Cys Lys Ala
92 115 120 125
94 Asp Tyr Glu Thr Ala Lys Gln Arg Glu Ala Glu Ala Thr Ala Lys Arg
95 130 135 140
97 Pro Arg Thr Thr Ile Thr Ala Lys Gln Leu Glu Thr Leu Lys Ser Ala
98 145 150 155 160
100 Tyr Asn Thr Ser Pro Lys Pro Ala Arg His Val Arg Glu Gln Leu Ser
101 165 170 175
103 Ser Glu Thr Gly Leu Asp Met Arg Val Val Gln Val Trp Phe Gln Asn
104 180 185 190
106 Arg Arg Ala Lys Glu Lys Arg Leu Lys Lys Asp Ala Gly Arg Gln Arg
107 195 200 205
109 Trp Gly Gln Tyr Phe Arg Asn Met Lys Arg Ala Arg Gly Gly Ser Lys
110 210 215 220
112 Ser Asp Lys Asp Ser Val Gln Glu Glu Gly Gln Asp Ser Asp Ala Glu
113 225 230 235 240
115 Val Ser Phe Thr Asp Glu Pro Ser Met Ala Glu Met Gly Pro Ala Asn
116 245 250 255
118 Gly Leu Tyr Gly Gly Leu Gly Glu Pro Ala Pro Ala Leu Gly Arg Pro
119 260 265 270
121 Ser Gly Ala Pro Gly Ser Phe Pro Leu Glu His Gly Gly Leu Ala Gly
122 275 280 285
124 Pro Glu Gln Tyr Gly Glu Leu Arg Pro Ser Ser Pro Tyr Gly Val Pro

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125      290      295      300
127 Ser Ser Pro Ala Ala Leu Gln Ser Leu Pro Gly Pro Gln Pro Leu Leu
128 305      310      315      320
130 Ser Ser Leu Val Tyr Pro Glu Ala Gly Leu Gly Leu Val Pro Ala Gly
131      325      330      335
133 Pro Pro Gly Gly Pro Pro Pro Met Arg Val Leu Ala Gly Asn Gly Pro
134      340      345      350
136 Ser Ser Asp Leu Ser Thr Gly Ser Ser Gly Gly Tyr Pro Asp Phe Pro
137      355      360      365
139 Ala Ser Pro Ala Ser Trp Leu Asp Glu Val Asp His Ala Gln Phe
140      370      375      380
143 <210> SEQ ID NO: 3
144 <211> LENGTH: 399
145 <212> TYPE: PRT
146 <213> ORGANISM: Mus musculus
148 <400> SEQUENCE: 3
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150 1      5      10      15
152 Pro Gly Ala Ser Ala Leu Cys Thr Phe Ser Arg Thr Pro Glu Ile Pro
153      20      25      30
155 Met Cys Ala Gly Cys Asp Gln His Ile Leu Asp Arg Phe Ile Leu Lys
156      35      40      45
158 Ala Leu Asp Arg His Trp His Ser Lys Cys Leu Lys Cys Ser Asp Cys
159      50      55      60
161 His Val Pro Leu Ala Glu Arg Cys Phe Ser Arg Gly Glu Ser Val Tyr
162 65      70      75      80
164 Cys Lys Asp Asp Phe Phe Lys Arg Phe Gly Thr Lys Cys Ala Ala Cys
165      85      90      95
167 Gln Leu Gly Ile Pro Pro Thr Gln Val Val Arg Arg Ala Gln Asp Phe
168      100      105      110
170 Val Tyr His Leu His Cys Phe Ala Cys Val Val Cys Lys Arg Gln Leu
171      115      120      125
173 Ala Thr Gly Asp Glu Phe Tyr Leu Met Glu Asp Ser Arg Leu Val Cys
174      130      135      140
176 Lys Ala Asp Tyr Glu Thr Ala Lys Gln Arg Glu Ala Glu Ala Thr Ala
177 145      150      155      160
179 Lys Arg Pro Arg Thr Thr Ile Thr Ala Lys Gln Leu Glu Thr Leu Lys
180      165      170      175
182 Ser Ala Tyr Asn Thr Ser Pro Lys Pro Ala Arg His Val Arg Glu Gln
183      180      185      190
185 Leu Ser Ser Glu Thr Gly Leu Asp Arg Val Val Gln Val Trp Phe Gln
186      195      200      205
188 Asn Arg Arg Ala Lys Glu Lys Arg Leu Lys Lys Asp Ala Gly Arg Gln
189      210      215      220
191 Arg Trp Gly Gln Tyr Phe Arg Asn Met Lys Arg Ser Arg Gly Ser Ser
192 225      230      235      240
194 Lys Ser Asp Lys Asp Ser Ile Gln Glu Gly Gln Asp Ser Asp Ala Glu
195      245      250      255
197 Val Ser Phe Thr Asp Glu Pro Ser Met Ala Asp Met Gly Pro Ala Asn

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198          260          265          270
200 Gly Leu Tyr Ser Ser Leu Gly Glu Pro Ala Pro Ala Leu Gly Arg Pro
201          275          280          285
203 Val Gly Gly Leu Gly Ser Phe Thr Leu Asp His Gly Gly Leu Thr Gly
204          290          295          300
206 Pro Glu Gln Tyr Arg Glu Leu Arg Pro Gly Ser Pro Tyr Gly Ile Pro
207 305          310          315          320
209 Pro Ser Pro Ala Ala Pro Gln Ser Leu Pro Gly Pro Gln Pro Leu Leu
210          325          330          335
212 Ser Ser Leu Val Tyr Pro Asp Thr Asn Leu Ser Leu Val Pro Ser Gly
213          340          345          350
215 Pro Pro Gly Gly Pro Pro Pro Met Arg Val Leu Ala Gly Asn Gly Pro
216          355          360          365
218 Ser Ser Asp Leu Ser Thr Glu Ser Ser Ser Gly Tyr Pro Asp Phe Pro
219          370          375          380
221 Ala Ser Pro Ala Ser Trp Leu Asp Glu Val Asp His Ala Gln Phe
222 385          390          395
225 <210> SEQ ID NO: 4
226 <211> LENGTH: 395
227 <212> TYPE: PRT
228 <213> ORGANISM: Gallus gallus
230 <400> SEQUENCE: 4
231 Met Leu Leu Glu Arg Val Arg Ala Gly Ser Glu Lys Ala Ala Glu Leu
232 1          5          10          15
234 Cys Pro Phe Pro Arg Ser Pro Glu Ile Pro Leu Cys Ala Gly Cys Asn
235          20          25          30
237 Gln His Ile Val Asp Arg Phe Ile Leu Lys Val Leu Asp Arg His Trp
238          35          40          45
240 His Ser Lys Cys Leu Lys Cys Ser Asp Cys Gln Thr Gln Leu Ala Glu
241          50          55          60
243 Lys Cys Phe Ser Arg Gly Asp Gly Val Tyr Cys Lys Glu Asp Phe Phe
244 65          70          75          80
246 Lys Arg Phe Gly Thr Lys Cys Ala Ala Cys Gln Gln Gly Ile Pro Pro
247          85          90          95
249 Thr Gln Val Val Arg Arg Ala Gln Asp Phe Val Tyr His Leu His Cys
250          100          105          110
252 Phe Ala Cys Ile Val Cys Lys Arg Gln Leu Ala Thr Gly Asp Glu Phe
253          115          120          125
255 Tyr Leu Met Glu Asp Ser Arg Leu Val Cys Lys Ala Asp Tyr Glu Thr
256          130          135          140
258 Ala Lys Gln Arg Glu Ala Glu Ser Thr Ala Lys Arg Pro Arg Thr Thr
259 145          150          155          160
261 Ile Thr Ala Lys Gln Leu Glu Thr Leu Lys Asn Ala Tyr Asn Asn Ser
262          165          170          175
264 Pro Lys Pro Ala Arg His Val Arg Glu Gln Leu Ser Ser Glu Thr Gly
265          180          185          190
267 Leu Asp Met Arg Val Val Gln Val Trp Phe Gln Asn Arg Arg Ala Lys
268          195          200          205
270 Glu Lys Arg Leu Lys Lys Asp Ala Gly Arg Gln Arg Trp Gly Gln Tyr

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271      210      215      220
273 Phe Arg Asn Met Lys Arg Ser Arg Gly Thr Ser Lys Ser Asp Lys Asp
274 225      230      235      240
276 Ser Ile Gln Glu Glu Gly Pro Asp Ser Asp Ala Glu Val Ser Phe Thr
277      245      250      255
279 Asp Glu Pro Ser Met Ser Glu Met Ser His Ser Asn Gly Ile Tyr Ser
280      260      265      270
282 Asn Leu Ser Glu Ala Ser Pro Ala Leu Gly Arg Gln Ala Gly Thr Asn
283      275      280      285
285 Gly Gly Phe Ser Leu Asp His Ser Gly Ile Pro Ala Gln Asp Gln Tyr
286      290      295      300
288 His Asp Leu Arg Ser Asn Ser Pro Tyr Gly Ile Pro Gln Ser Pro Ala
289 305      310      315      320
291 Ser Leu Gln Ala Leu Pro Gly His Gln Pro Leu Ile Ser Ser Leu Val
292      325      330      335
294 Tyr Pro Asp Ser Gly Leu Gly Ile Met Gly Gln Gly Gly Gln Gly Val
295      340      345      350
297 Pro Gln Ser Met Arg Val Leu Ala Gly Asn Gly Pro Ser Ser Asp Leu
298      355      360      365
300 Ser Thr Gly Ser Ser Gly Gly Tyr Pro Asp Phe Pro Ala Ser Pro Ala
301      370      375      380
303 Ser Trp Leu Asp Glu Val Asp His Ala Gln Phe
304 385      390      395
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308 <211> LENGTH: 394
309 <212> TYPE: PRT
310 <213> ORGANISM: Xenopus laevis
312 <400> SEQUENCE: 5
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314 1      5      10      15
316 Cys Gly Tyr Thr Gly Ser Pro Glu Ile Pro Gln Cys Ala Gly Cys Asn
317      20      25      30
319 Gln His Ile Val Asp Arg Phe Ile Leu Lys Val Leu Asp Arg His Trp
320      35      40      45
322 His Ser Lys Cys Leu Lys Cys Asn Asp Cys Gln Ile Gln Leu Ala Glu
323      50      55      60
325 Lys Cys Phe Ser Arg Gly Asp Ser Val Tyr Cys Lys Asp Asp Phe Phe
326 65      70      75      80
328 Lys Arg Phe Gly Thr Lys Cys Ala Ala Cys Gln Gln Gly Ile Pro Pro
329      85      90      95
331 Thr Gln Val Val Arg Arg Ala Gln Glu Phe Val Tyr His Leu His Cys
332      100      105      110
334 Phe Ala Cys Ile Val Cys Lys Arg Gln Leu Ala Thr Gly Asp Glu Phe
335      115      120      125
337 Tyr Leu Met Glu Asp Ser Arg Leu Val Cys Lys Ala Asp Tyr Glu Thr
338      130      135      140
340 Ala Lys Gln Arg Glu Ala Glu Ser Thr Ala Lys Arg Pro Arg Thr Thr
341 145      150      155      160
343 Ile Thr Ala Lys Gln Leu Glu Thr Leu Lys Asn Ala Tyr Asn Asn Ser

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 02/13/2002

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TIME: 18:44:30

Input Set : A:\053844-5003.txt

Output Set: N:\CRF3\02132002\I932367A.raw

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L:473 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:477 M:283 W: Missing Blank Line separator, <400> field identifier
L:478 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:980 M:283 W: Missing Blank Line separator, <400> field identifier
L:981 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:985 M:283 W: Missing Blank Line separator, <400> field identifier
L:986 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:1319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1602 M:283 W: Missing Blank Line separator, <400> field identifier
L:1603 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (30) SEQUENCE:
L:1620 M:283 W: Missing Blank Line separator, <400> field identifier
L:1621 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (32) SEQUENCE: